

06 May 2005

Alignment Results

Alignment: Global DNA alignment against reference molecule
 Parameters: Scoring matrix: Linear (Mismatch 2, OpenGap 4, ExtGap 1)

Reference molecule: SEQIDNO:5, Region 1-1356
 Number of sequences to align: 2
 Settings: Similarity significance value cutoff: >= 60%



Summary of Percent Matches:

Reference:	SEQIDNO:5	1 - 1356	(1356 bps)	--
Sequence 2:	Kimura Tri101	135 - 1490	(1356 bps)	99%

SEQIDNO:5	1	atggctttcaagatacagctcgacaccctcggccagctaccaggcctcctttcgatctac
Kimura Tri10	135	atggctttcaagatacagctcgacaccctcggccagctaccaggcctcctttcgatctac
SEQIDNO:5	61	acccaaatcagctctcctctaccccgctctctgattcctctcaatatccactattgtcagc
Kimura Tri10	195	acccaaatcagctctcctctaccccgctctctgattcctctcaatatccactattgtcagc
SEQIDNO:5	121	accttcgagcaaggctcttaagcgcttctccgaagccgtcccatgggtcgaggccaggtc
Kimura Tri10	255	accttcgagcaaggctcttaagcgcttctccgaagccgtcccatgggtcgaggccaggtc
SEQIDNO:5	181	aaagccgagggcattagcgagggaaacacaggaacttcctttatcgctcccttttgaggac
Kimura Tri10	315	aaagccgagggcattagcgagggaaacacaggaacttcctttatcgctcccttttgaggac
SEQIDNO:5	241	gttcctcgtgttgtagtgaaagacctccgcgatgatccttcagcgccacgatcgagggt
Kimura Tri10	375	gttcctcgtgttgtagtgaaagacctccgcgatgatccttcagcgccacgatcgagggt
SEQIDNO:5	301	atgagaaaggcgggataccctatggcgatgtttgacgagaacatcatcgcgccaaggaag
Kimura Tri10	435	atgagaaaggcgggataccctatggcgatgtttgacgagaacatcatcgcgccaaggaag
SEQIDNO:5	361	acgttacctattggacctggtagtggccccgacgacccaaagcctgtgaattctattgcag
Kimura Tri10	495	acgttacctattggacctggtagtggccccgacgacccaaagcctgtgaattctattgcag
SEQIDNO:5	421	ctcaacttcatcaagggcggactcatcctcactgtcaacggacagcacgggtgctatggat
Kimura Tri10	555	ctcaacttcatcaagggcggactcatcctcactgtcaacggacagcacgggtgctatggat
SEQIDNO:5	481	atggtaggccaagatgcggtgatccgtctactctccaaggcgtgccgtaacgacccattc
Kimura Tri10	615	atggtaggccaagatgcggtgatccgtctactctccaaggcgtgccgtaacgacccattc
SEQIDNO:5	541	accgaagaggaaatgacggccatgaacctcgatcgcaagacgatagttccttaccttgaa
Kimura Tri10	675	accgaagaggaaatgacggccatgaacctcgatcgcaagacgatagttccttaccttgaa
SEQIDNO:5	601	aactatacgattggccccgaggtagatcatcagattgtcaaagctgatgtagctggtggt
Kimura Tri10	735	aactatacgattggccccgaggtagatcatcagattgtcaaagctgatgtagctggtggt
SEQIDNO:5	661	gacgctgttctcacgcccgtcagtgcaagctggcggttcttcacattcagccccaaagcc
Kimura Tri10	795	gacgctgttctcacgcccgtcagtgcaagctggcggttcttcacattcagccccaaagcc
SEQIDNO:5	721	atgtcagagctcaaggatgctgctaccaagactcttgacgcatcaacaaagttcgtgtcg
Kimura Tri10	855	atgtcagagctcaaggatgctgctaccaagactcttgacgcatcaacaaagttcgtgtcg
SEQIDNO:5	781	actgacgatgctctttcggcggttcattctggaaatcggcctctcgcggtgctctcgaaaga
Kimura Tri10	915	actgacgatgctctttcggcggttcattctggaaatcggcctctcgcggtgctctcgaaaga
SEQIDNO:5	841	atcgatggctctgcacctaccgagttctgccgtgctgttgatgctcgaccggcaatgggt
Kimura Tri10	975	atcgatggctctgcacctaccgagttctgccgtgctgttgatgctcgaccggcaatgggt
SEQIDNO:5	901	gtctcgaacaactaccaggccttcttcaaaacatgacctaccacaactcgaccatcgcc
Kimura Tri10	1035	gtctcgaacaactaccaggccttcttcaaaacatgacctaccacaactcgaccatcgcc
SEQIDNO:5	961	gaaatcgccaacgagtcactcggcggaacagcatcacgccttcggttcagaactcgacccc
Kimura Tri10	1095	gaaatcgccaacgagtcactcggcggaacagcatcacgccttcggttcagaactcgacccc

SEQIDNO:5	1021	gcgagcatgcgccagcgaacaagaggtctcgcgacgtacctgcacaacaaccccgacaag
Kimura Tri10	1155	gcgagcatgcgccagcgaacaagaggtctcgcgacgtacctgcacaacaaccccgacaag
SEQIDNO:5	1081	tccaacgtatccctgacggctgatgcggaacctctaccagcgtcatgctgagttcttgg
Kimura Tri10	1215	tccaacgtatctctgacggctgatgcggaacctctaccagcgtcatgctgagttcttgg
SEQIDNO:5	1141	gccaaagtgggactctgggattacgactttgggctcggactgggtaagcccagactgtg
Kimura Tri10	1275	gccaaagtgggactctgggattacgactttgggctcggactgggtaagcccagactgtg
SEQIDNO:5	1201	agacggccaatctttgagcctggtgagagcttgatgtactttatgcccaagaagcctgat
Kimura Tri10	1335	agacggccaatctttgagcctggtgagagcttgatgtactttatgcccaagaagcctgat
SEQIDNO:5	1261	ggcgagttctgtgcggcgctttctctgagggatgaggatatggaccgattgaaggcggat
Kimura Tri10	1395	ggcgagttctgtgcggcgctttctctgagggatgaggatatggaccgattgaaggcggat
SEQIDNO:5	1321	aaggagtggaccaagtatgcgcagtagcttggttag
Kimura Tri10	1455	aaggagtggaccaagtatgcgcagtagcttggttag